

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 12:57:33 ; Search time 152 Seconds
(without alignments)
54.281 Million cell updates/sec

Title: US-09-868-300-8_COPY_96_118
Perfect score: 115
Sequence: 1 VLHIELRRWADWMIAPLSANTL 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	217	3 AAY96816	A. thalia
2	111	96.5	199	3 AAG11382	Aag11382 Arabidops
3	111	96.5	209	3 AAG11381	Aag11381 Arabidops
4	111	96.5	209	8 ADN73067	Adn73067 Thale cre
5	106	92.2	648	7 ADF75109	Adf75109 A goesypi
6	106	92.2	674	7 ADK62474	Adk62474 Disease t
7	99	86.1	170	4 AAU18952	Aau18952 Novel lun
8	99	86.1	170	4 AAU17967	Aau17967 Novel hum
9	99	86.1	170	6 ABU66558	Abu66558 Human lun
10	99	86.1	170	7 ADB96723	Adb96723 Novel lun
11	99	86.1	170	7 ADG41347	Adg41347 Human res
12	99	86.1	204	4 AAM39470	Aam39470 Human pol
13	99	86.1	204	4 AAB94179	Aab94179 Human pro
14	99	86.1	309	4 ABB11631	Abb11631 Human rec
15	99	86.1	309	4 AAM41256	Aam41256 Human pol
16	99	86.1	326	3 AAY32199	Aay32199 Human rec
17	96	83.5	571	6 ABR52911	AbR52911 Protein s
18	96	83.5	571	7 ADK62458	Adk62458 Disease t
19	78	67.8	427	6 ADA33918	Ada33918 Acinetoba
20	76	66.1	431	8 ADL05850	Adl05850 M. catar
21	71	61.7	399	5 ABB47692	Abb47692 Listeria
22	71	61.7	405	7 ABO75311	Abo75311 Pseudomon
23	69	60.0	399	4 AAG82741	Aag82741 S. epider
24	69	60.0	400	5 ABP39940	Abp39940 Staphyloc
25	69	60.0	401	6 ABM71249	Abm71249 Staphyloc

ALIGNMENTS

RESULT 1

AAV96816	26	69	60.0	428	6	ABM68817	Abm68817 Photorhab
ID AAY96816 standard; protein; 217 AA.	27	68	59.1	376	7	ADM26107	Adm26107 Hyperther
XX AC AAY96816;	28	67	58.3	398	7	ABO64139	AbO64139 Klebeieil
XX DT 26-SEP-2000 (first entry)	29	67	58.3	430	6	ABR63491	AbR63491 E coli fl
XX DE A. thaliana Vb89 (HAL3) CDC2b interacting protein.	30	67	58.3	430	6	ABR63492	AbR63492 E coli fl
XX KW Cyclin-dependent protein kinase; CDK; CDC2a; CDC2b; Vb89; HAL3;	31	65	56.5	188	5	ABO09642	AbO09642 MutD prot
XX KW cell cycle; interacting protein; environmental stress; growth regulator;	32	65	56.5	188	6	ABG72540	Abg72540 Streptoco
XX KW herbicide; nematode resistance; plant breeding.	33	65	56.5	401	6	ADB10278	AdB10278 Alloiocec
XX OS Arabidopsis thaliana.	34	65	56.5	401	8	ADJ27133	AdJ27133 Alloiocec
XX PN WO200036124-A2.	35	65	56.5	418	7	ADF07150	Adf07150 Bacterial
XX PD 22-JUN-2000.	36	64	55.7	180	5	ABP28493	AbP28493 Streptoco
XX PF 17-DEC-1999; 99WO-EP010084.	37	64	55.7	181	5	ABP28494	AbP28494 Streptoco
XX PR 17-DEC-1998; 98EP-00124062.	38	61	53.0	183	6	ABU01661	AbU01661 S. pneumo
(CROP-) CROPDESIGN NV.	39	61	53.0	183	6	ABP81597	AbP81597 Streptoco
De Veylder L, Boudolf VKCK, Torres Acosta JA, Inze D;	40	61	53.0	183	8	ADK48063	AdK48063 Streptoco
WPI; 2000-431601/37.	41	61	53.0	394	6	ABP80942	AbP80942 N. gonorr
N-PSDB; AAA51412.	42	59	51.3	188	7	ADC97191	AdC97191 E. faeciu
Nucleic acids encoding plant cell cycle interacting proteins, useful for	43	51	44.3	228	2	AAW98418	Aaw98418 H. pylori
regulating plant growth and in recombinant DNA protocols.	44	49	42.6	269	4	AAU63490	Aau63490 Propionib
Claim 1; Page 126; 152pp; English.	45	49	42.6	269	6	ABM60009	Abm60009 Propionib
The Vb89 clone encodes the Arabidopsis thaliana HAL3 homologue, a							
halotolerant gene isolated in Saccharomyces cerevisiae. The Vb89 clone							
interacts with A. thaliana CDC2b (a cyclin-dependent protein kinase							
(CDK)), but not with CDC2a in the two-hybrid system. CDC2a and CDC2b							
are the only CDK genes to have been characterized in detail in							
Arabidopsis thaliana. They were used as bait in a two-hybrid screening							
assay with a cDNA library of a plant cell suspension as prey. The plant							
cell cycle interacting proteins identified were designated Ldv115, PHO80-							
like protein, Vb33, Vb89, VbDAHP and VbHSP. The nucleic acids, vectors							
comprising them, the proteins they express, antibodies that bind to them							
and/or inhibitors of their protein expression and/or activity may be used							
for modulating the cell cycle in an animal or plant, plant cell division							

CC and/or growth, for influencing the activity of cell cycle proteins in a
CC plant or animal cell, as positive or negative regulators of cell
CC proliferation, for modifying the growth inhibition caused by
CC environmental stress conditions (e.g. to improve growth of plants in
CC normal or suboptimal nutrient conditions, especially phosphorus), for use
CC in a screening method for inhibitors or activators of cell cycle protein,
CC as growth regulators, herbicides and/or for inducing nematode resistance
CC in plants. The DNA sequences and their regulatory sequences may be used
CC as markers in plant or animal cell and tissue cultures or as a marker in
CC marker-assisted plant breeding. The regulatory sequences may also be used
CC for the expression of heterologous DNA sequences during a stage of the
CC cell cycle
XX
SQ Sequence 217 AA;

Query Match 100.0%; Score 115; DB 3; Length 217;
Best Local Similarity 100.0%; Pred. No. 1.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADWMIAPLSANTL 23
|||
Db 96 VLHIELRWADWMIAPLSANTL 118

RESULT 2

AG11382
ID AAG11382 standard; protein; 199 AA.

AC AAG11382;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 10077.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 10077.
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

XX Arabidopsis thaliana.

OS EP1033405-A2.

PN 06-SEP-2000.

PD 25-FEB-2000; 2000EP-00301439.

PF 25-FEB-1999; 99US-0121825P.

XX 05-MAR-1999; 99US-0123180P.

PR 09-MAR-1999; 99US-0123548P.

PR 23-MAR-1999; 99US-0125788P.

PR 25-MAR-1999; 99US-0126264P.

PR 29-MAR-1999; 99US-0126785P.

PR 01-APR-1999; 99US-0127462P.

PR 06-APR-1999; 99US-0128234P.

PR 08-APR-1999; 99US-0128714P.

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PR 19-APR-1999; 99US-0130077P.

PR 21-APR-1999; 99US-0130449P.

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Best Local Similarity 91.3%; Pred. No. 7e-11;		
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0		
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Db	78	VLHIELRRWADYMIAPLSANTL 100
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RESULT 3		
AGL1381	Arabidopsis thaliana protein fragment SEQ ID NO: 10076.	
ID	AAG11381 standard; protein; 209 AA.	
XX	AC AAG11381;	
XX	DT 17-OCT-2000 (first entry)	
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 10076.	
KW	Protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
KW	termination sequence.	
XX	Arabidopsis thaliana.	
XX	EP1033405-A2.	
PD	06-SEP-2000.	
XX	25-FEB-2000; 2000EP-00301439.	
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Query Match	96.5%;	Score 111;	DB 8;	Length 209;
Best Local Similarity	91.3%;	Pred. No. 7.4e-11;		

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PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 13-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239935P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
PR 08-NOV-2000; 2000US-0246474P.
PR 08-NOV-2000; 2000US-0246475P.
PR 08-NOV-2000; 2000US-0246476P.
PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
PR 08-NOV-2000; 2000US-0246524P.
PR 08-NOV-2000; 2000US-0246525P.
PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
PR 08-NOV-2000; 2000US-0246532P.
PR 08-NOV-2000; 2000US-0246609P.
PR 08-NOV-2000; 2000US-0246610P.
PR 08-NOV-2000; 2000US-0246611P.
PR 08-NOV-2000; 2000US-0246613P.
PR 17-NOV-2000; 2000US-0249207P.
PR 17-NOV-2000; 2000US-0249208P.
PR 17-NOV-2000; 2000US-0249210P.
PR 17-NOV-2000; 2000US-0249211P.
PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
PR 17-NOV-2000; 2000US-0249218P.
PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249264P.
PR 17-NOV-2000; 2000US-0249265P.
PR 17-NOV-2000; 2000US-0249297P.
PR 17-NOV-2000; 2000US-0249299P.
PR 17-NOV-2000; 2000US-0249300P.
PR 01-DEC-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0251479P.

PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 08-DEC-2000; 2000US-0251990P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI Rosen CA, Barash SC, Ruben SM;
XX WPI; 2001-465565/50.
XX N-PSDB; AAS30612.
PT Isolated nucleic acid molecule encoding a lung cancer antigen is used in
PT preventing, treating or ameliorating a medical condition.
XX Claim 1; SEQ ID NO 64; 475pp; English.
XX The invention relates to novel isolated lung cancer antigen
CC polynucleotides (I) and polypeptides (II). (I) and (II) are used to
CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC rabbits, goats, horses, cats, dogs, chickens or sheep. (I) and (II) are
CC also used in diagnosing a pathological condition or susceptibility to a
CC pathological condition, in particular, lung cancer. The antibodies to
CC (II) can also be used in alleviating symptoms associated with the
CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
CC treated include autoimmune diseases e.g. rheumatoid arthritis,
CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
CC ocular disorders e.g. corneal infection. The polypeptides can also be
CC used to aid wound healing and epithelial cell proliferation, to prevent
CC skin aging due to sunburn, to maintain organs before transplantation, for
CC supporting cell culture of primary tissues, to regenerate tissues and in
CC chemotaxis. AAU18928-AAU18958 represent novel human lung cancer antigen
CC amino acid sequences, and related sequences of the invention. Note: The
CC sequence data for this patent did not form part of the printed from WIPO
CC specification, but was obtained in electronic format directly from WIPO
XX at: ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 170 AA;

Query Match 86.1%; Score 99; DB 4; Length 170;
Best Local Similarity 73.9%; Pred. No. 7.3e-09;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLHTELRWADWMIITAPLSANTL 23
Db 52 VLHIDRRWADLLVAPLDANTL 74
||||:|||||:|||||
||||:|||||:|||||

RESULT 8
AAU17967
ID AAU17967 standard; protein; 170 AA.
XX AC AAU17967;
XX DT 07-NOV-2001 (first entry)
XX DE Novel human respiratory antigen #283.
XX Human; respiratory antigen; respiratory disorder; throat disorder;
KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;
KW anti allergic; anti asthmatic; anti inflammatory; olfactory;
XX respiratory active.
XX OS Homo sapiens.
XX PN WO200155448-A1.

XX	02-AUG-2001.	PR	29-SEP-2000;	2000US-0236367P.
PD		PR	29-SEP-2000;	2000US-0236368P.
XX		PR	29-SEP-2000;	2000US-0236369P.
PF	17-JAN-2001;	PR	29-SEP-2000;	2000US-0236370P.
XX	2001WO-US001333.	PR	02-OCT-2000;	2000US-0236802P.
		PR	02-OCT-2000;	2000US-0237037P.
		PR	02-OCT-2000;	2000US-0237038P.
		PR	02-OCT-2000;	2000US-0237039P.
		PR	02-OCT-2000;	2000US-0237040P.
		PR	13-OCT-2000;	2000US-0239933P.
		PR	13-OCT-2000;	2000US-0239937P.
		PR	20-OCT-2000;	2000US-0240960P.
		PR	20-OCT-2000;	2000US-0241221P.
		PR	20-OCT-2000;	2000US-0241785P.
		PR	20-OCT-2000;	2000US-0241786P.
		PR	20-OCT-2000;	2000US-0241787P.
		PR	20-OCT-2000;	2000US-0241808P.
		PR	20-OCT-2000;	2000US-0241809P.
		PR	20-OCT-2000;	2000US-0241825P.
		PR	01-NOV-2000;	2000US-0244617P.
		PR	08-NOV-2000;	2000US-0246474P.
		PR	08-NOV-2000;	2000US-0246475P.
		PR	08-NOV-2000;	2000US-0246476P.
		PR	08-NOV-2000;	2000US-0246477P.
		PR	08-NOV-2000;	2000US-0246478P.
		PR	08-NOV-2000;	2000US-0246523P.
		PR	08-NOV-2000;	2000US-0246524P.
		PR	08-NOV-2000;	2000US-0246525P.
		PR	08-NOV-2000;	2000US-0246526P.
		PR	08-NOV-2000;	2000US-0246527P.
		PR	08-NOV-2000;	2000US-0246528P.
		PR	08-NOV-2000;	2000US-0246532P.
		PR	08-NOV-2000;	2000US-0246609P.
		PR	08-NOV-2000;	2000US-0246610P.
		PR	08-NOV-2000;	2000US-0246611P.
		PR	08-NOV-2000;	2000US-0246613P.
		PR	17-NOV-2000;	2000US-0249207P.
		PR	17-NOV-2000;	2000US-0249208P.
		PR	17-NOV-2000;	2000US-0249209P.
		PR	17-NOV-2000;	2000US-0249210P.
		PR	17-NOV-2000;	2000US-0249211P.
		PR	17-NOV-2000;	2000US-0249212P.
		PR	17-NOV-2000;	2000US-0249213P.
		PR	17-NOV-2000;	2000US-0249214P.
		PR	17-NOV-2000;	2000US-0249215P.
		PR	17-NOV-2000;	2000US-0249216P.
		PR	17-NOV-2000;	2000US-0249217P.
		PR	17-NOV-2000;	2000US-0249218P.
		PR	17-NOV-2000;	2000US-0249244P.
		PR	17-NOV-2000;	2000US-0249245P.
		PR	17-NOV-2000;	2000US-0249264P.
		PR	17-NOV-2000;	2000US-0249265P.
		PR	17-NOV-2000;	2000US-0249297P.
		PR	17-NOV-2000;	2000US-0249299P.
		PR	17-NOV-2000;	2000US-0249300P.
		PR	01-DEC-2000;	2000US-0250160P.
		PR	01-DEC-2000;	2000US-0250391P.
		PR	05-DEC-2000;	2000US-0251030P.
		PR	05-DEC-2000;	2000US-0251988P.
		PR	05-DEC-2000;	2000US-0256719P.
		PR	06-DEC-2000;	2000US-0251479P.
		PR	08-DEC-2000;	2000US-0251856P.
		PR	08-DEC-2000;	2000US-0251868P.
		PR	08-DEC-2000;	2000US-0251869P.
		PR	08-DEC-2000;	2000US-0251989P.
		PR	08-DEC-2000;	2000US-0251990P.
		PR	11-DEC-2000;	2000US-0254097P.
		PR	05-JAN-2001;	2001US-0259678P.
		XX		
		PA	(HUMA-) HUMAN GENOME SCI	INC.
		XX		
		PI	Rosen CA, Barash SC, Ruben SM;	
		XX		

DR WPI; 2001-476224/51.
 DR N-PSDB; AAS28151.
 XX Isolated polypeptide for treating, preventing and/or prognosing
 PT disorders related to the respiratory system including respiratory cancers
 PT and also for testing and detection e.g. diagnosis.
 XX
 PS Claim 11; SED ID No 585; 545pp; English.
 XX
 CC The present invention relates to the isolation of novel human respiratory
 CC antigens, and cDNA (AAS27869-AAS28159) and genomic sequences encoding for
 CC these polypeptides. The sequences of the invention are useful for
 CC preventing, treating and/or prognosing disorders related to the
 CC respiratory system including throat disorders (e.g. vocal cord paralysis,
 CC tonsillitis, and laryngitis), lung disorders (e.g. pneumonia, allergic
 CC disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose
 CC disorders and cancers of the respiratory tissues e.g. lung cancer. The
 CC polynucleotide sequences of the invention are useful in gene therapy and
 CC antisense therapy. AAU17685-AAU17975 represent novel human respiratory
 CC antigens. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 170 AA;
 Query Match 86.1%; Score 99; DB 4; Length 170;
 Best Local Similarity 73.9%; Pred. No. 7.3e-09;
 Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
 QY 1 VLHILRRWADWMTIAPLSANTL 23
 DB 52 VLHILRRWADWMTIAPLSANTL 74
 RESULT 9
 ABU66558
 ID ABU66558 standard; protein; 170 AA.
 AC
 AC ABU66558;
 XX
 DT 22-MAY-2003 (first entry)
 XX
 DE Human lung cancer antigen HAABL43.
 XX
 KW Human; lung cancer antigen; anaemia; tissue regeneration; wound healing;
 KW constant region; immunotherapy; gene therapy; lung disorder; leukopenia;
 KW small cell lung cancer; squamous cell carcinoma; adenocarcinoma; asthma;
 KW respiratory disorder; nonallergic rhinitis; rheumatoid arthritis; ulcer;
 KW adult respiratory distress syndrome; hyperproliferative disorder; graft;
 KW lung neoplasm; prostate neoplasm; immune system disorder; anaphylaxis;
 KW multiple sclerosis; blood-related disorder; allergic reaction; impotence;
 KW inflammatory disorder; appendicitis; dermatitis; graft vs host disease;
 KW immune complex disease; serum sickness; polyarteritis nodosa; arrhythmia;
 KW urinary system disorder; glomerulonephritis; kidney failure; infertility;
 KW cardiovascular disorder; myocardial infarction; osteoarthritis; aging;
 KW musculoskeletal system disorder; Albers-Schonberg disease; cancer; burn;
 KW neurological disorder; Alzheimer's disease; Parkinson's disease; trauma;
 KW endocrine disorder; Addison's disease; diabetes mellitus; gastric reflux;
 KW gastrointestinal disorder; reproductive system disorder; cerebral palsy;
 KW developmental disorder; Fanconi's syndrome; cellular level disease;
 KW amyotrophic lateral sclerosis; infectious disease; viral infection;
 KW bacterial infection.
 XX
 OS Homo sapiens.
 XX
 PN US2002173454-A1.
 XX
 PD 21-NOV-2002.
 XX
 PP 17-JAN-2001; 2001US-00764904.
 XX
 XX 31-JAN-2000; 2000US-0179065P.
 PR 04-FEB-2000; 2000US-0180628P.

PR 28-JUN-2000; 2000US-0214886P.
 PR 07-JUL-2000; 2000US-0216647P.
 PR 07-JUL-2000; 2000US-0216880P.
 PR 11-JUL-2000; 2000US-0217487P.
 PR 11-JUL-2000; 2000US-0217496P.
 PR 14-JUL-2000; 2000US-0218290P.
 PR 26-JUL-2000; 2000US-0220963P.
 PR 26-JUL-2000; 2000US-0220964P.
 PR 14-AUG-2000; 2000US-0224518P.
 PR 14-AUG-2000; 2000US-0224519P.
 PR 14-AUG-2000; 2000US-0225267P.
 PR 14-AUG-2000; 2000US-0225268P.
 PR 14-AUG-2000; 2000US-0225270P.
 PR 14-AUG-2000; 2000US-0225447P.
 PR 14-AUG-2000; 2000US-0225757P.
 PR 14-AUG-2000; 2000US-0225758P.
 PR 22-AUG-2000; 2000US-0226868P.
 PR 30-AUG-2000; 2000US-0228924P.
 PR 01-SEP-2000; 2000US-0229287P.
 PR 01-SEP-2000; 2000US-0229343P.
 PR 01-SEP-2000; 2000US-0229344P.
 PR 05-SEP-2000; 2000US-0229509P.
 PR 05-SEP-2000; 2000US-0229513P.
 PR 08-SEP-2000; 2000US-0231413P.
 PR 21-SEP-2000; 2000US-0234223P.
 PR 21-SEP-2000; 2000US-0234274P.
 PR 25-SEP-2000; 2000US-0234997P.
 PR 27-SEP-2000; 2000US-0235834P.
 PR 29-SEP-2000; 2000US-0236327P.
 PR 29-SEP-2000; 2000US-0236367P.
 PR 29-SEP-2000; 2000US-0236368P.
 PR 29-SEP-2000; 2000US-0236369P.
 PR 29-SEP-2000; 2000US-0236370P.
 PR 02-OCT-2000; 2000US-0236802P.
 PR 02-OCT-2000; 2000US-0237037P.
 PR 02-OCT-2000; 2000US-0237038P.
 PR 02-OCT-2000; 2000US-0237039P.
 PR 13-OCT-2000; 2000US-0239935P.
 PR 20-OCT-2000; 2000US-0240960P.
 PR 20-OCT-2000; 2000US-0241785P.
 PR 20-OCT-2000; 2000US-0241809P.
 PR 01-NOV-2000; 2000US-0244617P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 08-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 (ROSE/) ROSEN C A.
 (RUBE/) RUBEN S M.
 (BARA/) BARASH S C.
 Rosen CA, Ruben SM, Barash SC;
 WPI; 2003-311001/30.
 N-PSDB; ACA03375.
 Novel lung cancer related polypeptide useful for detecting, treating,
 preventing and/or prognosing lung, respiratory, hyperproliferative,
 immune system, cardiovascular endocrine or gastrointestinal disorders.
 Claim 11; Page 185; 332pp; English.
 The invention relates to an isolated lung cancer related polypeptide its
 variants, allelic variants or homologues. The polypeptide and its nucleic
 acid are useful for preventing, treating, or ameliorating a medical
 condition in a mammalian subject, for diagnosing a pathological condition
 or a susceptibility to a pathological condition in a subject by
 determining the presence or absence of mutation in the nucleic acid or
 determining the presence or amount of expression of the polypeptide in a
 biological sample and diagnosing a pathological condition based on the
 result. The polypeptide, antibodies to the polypeptide or the

CC polynucleotide are useful for detecting, treating, preventing and/or
CC prognosing disorders of the lung, such as small cell lung cancer, non-
CC large cell lung cancer (e.g. squamous cell carcinoma, adenocarcinoma,
CC carcinoma) or lung cancer metastasis. The polypeptide, its antibodies or
CC its polynucleotide are also useful for detecting, treating, preventing
CC and/or prognosing respiratory disorders e.g. nonallergic rhinitis and
CC adult respiratory distress syndrome; hyperproliferative disorders e.g.
CC lung neoplasms and prostate neoplasms; immune system disorders e.g.
CC rheumatoid arthritis and multiple sclerosis; blood-related disorders e.g.
CC anaemia and leukopenia; allergic reactions e.g. anaphylaxis and asthma;
CC inflammatory disorders e.g. appendicitis and dermatitis; graft vs host
CC disease; immune complex disease e.g. serum sickness and polyarthritis
CC nodosa; urinary system disorders e.g. glomerulonephritis and kidney
CC failure; cardiovascular disorders e.g. arrhythmia and myocardial
CC infarction; musculoskeletal system disorders e.g. Albers-Schonberg
CC disease and osteoarthritis; neurological disorders e.g. Alzheimer's
CC disease and Parkinson's disease; endocrine disorders e.g. Addison's
CC disease and diabetes mellitus; gastrointestinal disorders e.g. ulcers and
CC gastric reflux; reproductive system disorders e.g. infertility and
CC impotence; developmental and inherited disorders e.g. Fanconi's syndrome
CC and cerebral palsy; diseases at the cellular level e.g. cancer and
CC amyotrophic lateral sclerosis; infectious diseases e.g. viral and
CC bacterial. The polypeptide, its antibodies or its polynucleotide are also
CC useful for wound healing e.g. grafts and burns and for regeneration of
CC tissues damaged due to e.g. aging and trauma. The present sequence
CC represents the amino acid sequence of a human lung cancer antigen
XX
SQ Sequence 170 AA;

Query Match 86.1%; Score 99; DB 6; Length 170;
Best Local Similarity 73.9%; Pred. No. 7.3e-09;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHILRRWADVIITAPISANTL 23
Db 52 VLHILRRWADLLVAPLDANTL 74
|||||:|||||:|||||
|||||:|||||:|||||

RESULT 10
ADB96723
ID ADB96723 standard; protein; 170 AA.
AC ADB96723;
XX
XX 04-DEC-2003 (first entry)
XX
XX Novel lung cancer antigen polypeptide #24.
KW lung disorder; small cell lung cancer; non-small cell lung cancer;
KW adenocarcinoma; lung cancer metastasis; hyperproliferative disorder;
KW respiratory disorder; nonallergic rhinitis; sinusitis; bronchiolitis;
KW infiltrative lung disease; Goodpasture's syndrome; pneumonia;
KW immune system disorder; immunodeficiency; Chediak Higashi syndrome;
KW autoimmune disorder; rheumatoid arthritis; systemic lupus erythematosus;
KW multiple sclerosis; autoimmune haemolytic anaemia;
KW insulin-dependent diabetes mellitus; type II collagen induced arthritis;
KW dermatitis; eye disorder; scleroderma; chronic active hepatitis;
KW primary biliary cirrhosis; vitiligo; vasculitis; urticaria; asthma;
KW inflammatory disorder; granulomatous disorder; degenerative disorder;
KW atrophic disorder; haematopoietic cell disorder; thrombocytopenia;
KW leukopenia; anaemia; neutropenia; anaphylaxis;
KW blood group incompatibility; allergy; inflammatory bowel disease;
KW septic shock; sepsis; ischaemia-reperfusion injury; nephritis;
KW CNS disorder; stroke; neurodegenerative disorder; Alzheimer's disease;
KW Parkinson's disease; AIDS-related dementia; prion disease;
KW cardiovascular disease; atherosclerosis; organ transplant rejection;
KW blood-related disorder; vaccine; lung cancer antigen.
XX Homo sapiens.
OS
XX
XX US2003049703-A1.
PN
XX

29-SEP-2000; 2000US-0236368P.
29-SEP-2000; 2000US-0236369P.
29-SEP-2000; 2000US-0236370P.
02-OCT-2000; 2000US-0236802P.
02-OCT-2000; 2000US-0237037P.
02-OCT-2000; 2000US-0237038P.
02-OCT-2000; 2000US-0237039P.
02-OCT-2000; 2000US-0237040P.
13-OCT-2000; 2000US-0239935P.
13-OCT-2000; 2000US-0239937P.
20-OCT-2000; 2000US-0240960P.
20-OCT-2000; 2000US-0241221P.
20-OCT-2000; 2000US-0241785P.
20-OCT-2000; 2000US-0241786P.
20-OCT-2000; 2000US-0241787P.
20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241809P.
20-OCT-2000; 2000US-0241826P.
01-NOV-2000; 2000US-0244617P.
08-NOV-2000; 2000US-0246474P.
08-NOV-2000; 2000US-0246475P.
08-NOV-2000; 2000US-0246476P.
08-NOV-2000; 2000US-0246477P.
08-NOV-2000; 2000US-0246478P.
08-NOV-2000; 2000US-0246523P.
08-NOV-2000; 2000US-0246524P.
08-NOV-2000; 2000US-0246525P.
08-NOV-2000; 2000US-0246526P.
08-NOV-2000; 2000US-0246527P.
08-NOV-2000; 2000US-0246528P.
08-NOV-2000; 2000US-0246532P.
08-NOV-2000; 2000US-0246609P.
08-NOV-2000; 2000US-0246610P.
08-NOV-2000; 2000US-0246611P.
08-NOV-2000; 2000US-0246613P.
17-NOV-2000; 2000US-0249207P.
17-NOV-2000; 2000US-0249208P.
17-NOV-2000; 2000US-0249209P.
17-NOV-2000; 2000US-0249210P.
17-NOV-2000; 2000US-0249211P.
17-NOV-2000; 2000US-0249212P.
17-NOV-2000; 2000US-0249213P.
17-NOV-2000; 2000US-0249214P.
17-NOV-2000; 2000US-0249215P.
17-NOV-2000; 2000US-0249216P.
17-NOV-2000; 2000US-0249217P.
17-NOV-2000; 2000US-0249218P.
17-NOV-2000; 2000US-0249244P.
17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249265P.
17-NOV-2000; 2000US-0249266P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-0249299P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250391P.
05-DEC-2000; 2000US-0251030P.
05-DEC-2000; 2000US-0251988P.
05-DEC-2000; 2000US-0256719P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254907P.
05-JAN-2001; 2001US-0259678P.
17-JAN-2001; 2001US-00764904.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Ruben SM, Barash SC;
XX

DR WPI; 2003-695890/66.
DR N-PSDB; ADB96693.
XX
PT New lung cancer related polypeptide and polynucleotide, useful for
preventing, treating or ameliorating a medical condition, for example
PT cancer, HIV, and diabetes, and for diagnosing a pathological condition in
PT a subject.
XX
PS Claim 11; Page 184; 332pp; English.
XX
CC The invention describes an isolated lung cancer antigen polypeptide (I).
CC (I) or the polynucleotide (II) encoding it are useful for preventing,
CC treating or ameliorating a medical condition, in a subject. (I) is useful
CC for treating or preventing diseases or conditions of the lung, e.g. small
CC cell lung cancer, non-small cell lung cancer, adenocarcinoma and lung
CC cancer metastases. (I) is useful for treating hyperproliferative or
CC respiratory disorders. (II) or an anti-(I)-antibody is useful for
CC treating, preventing, diagnosing and/or prognosing diseases and/or
CC disorders of respiratory system (e.g. nonallergic rhinitis, sinusitis,
CC bronchiolitis, infiltrative lung disease, Goodpasture's syndrome and
CC pneumonia), disorders of immune system, congenital and acquired
CC immunodeficiencies (e.g. Chediak Higashi syndrome), and as an agent to

Query Match 86.1%; Score 99; DB 7; Length 170;
Best Local Similarity 73.9%; Pred. No. 7.3e-09;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 VLHLELRWADVMITAPLSANTL 23
DB 52 VLHIDLRWADLLLVAPLDANTL 74
|||:|||||:|||||
RESULT 11
ADG41347
ID ADG41347 standard; protein; 170 AA.
XX
AC ADG41347;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human respiratory system associated protein seq id 585.
XX
KW antiinflammatory; antiallergic; antiasthmatic; cytostatic; gene therapy;
KW respiratory system antigen;
KW human respiratory system associated polynucleotide;
KW respiratory system disorder; throat disorder; vocal cord paralysis;
KW tonsillitis; laryngitis; lung disorder; pneumonia; allergic disorder;
KW asthma; eosinophilic pneumonia; pleurisy; cystic fibrosis; emphysema;
KW histiocytosis; sarcoidosis; nose disorder; rhinitis; sinusitis; neoplasm;
KW cancer; respiratory tissue cancer; throat cancer; lung cancer;
KW cancer of the nose; gene therapy; chromosome identification; forensic;
KW human respiratory system associated protein; human.
XX
OS Homo sapiens.
XX
PN US2003215893-A1.
XX
PD 20-NOV-2003.
XX
PF 07-AUG-2002; 2002US-00212872.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-0205515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
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PR 07-JUL-2000; 2000US-0215880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.
PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225266P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225757P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226279P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226868P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
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PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
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PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
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PR 21-SEP-2000; 2000US-0234223P.
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PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235834P.
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PR 28-SEP-2000; 2000US-0235935P.
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PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239937P.
PR 20-OCT-2000; 2000US-0240360P.
PR 20-OCT-2000; 2000US-0241221P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 01-NOV-2000; 2000US-0244617P.
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PR 08-NOV-2000; 2000US-0246477P.
PR 08-NOV-2000; 2000US-0246478P.
PR 08-NOV-2000; 2000US-0246523P.
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PR 08-NOV-2000; 2000US-0246526P.
PR 08-NOV-2000; 2000US-0246527P.
PR 08-NOV-2000; 2000US-0246528P.
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PR 17-NOV-2000; 2000US-0249207P.
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PR 17-NOV-2000; 2000US-0249212P.
PR 17-NOV-2000; 2000US-0249213P.
PR 17-NOV-2000; 2000US-0249214P.
PR 17-NOV-2000; 2000US-0249215P.
PR 17-NOV-2000; 2000US-0249216P.
PR 17-NOV-2000; 2000US-0249217P.
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PR 17-NOV-2000; 2000US-0249244P.
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PR 17-NOV-2000; 2000US-0249265P.
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PR 01-DEC-2000; 2000US-0250160P.
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PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
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PR 06-DEC-2000; 2000US-0251479P.
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PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
PR 17-JAN-2001; 2001US-00764860.
PR 14-FEB-2002; 2002US-00074095.

XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM, Barash SC;

XX WPI; 2003-902033/82.

XX N-PSDB; ADG41055.

XX Novel respiratory system antigen and polynucleotides encoding the
PT polypeptides, useful for treating diagnosing, treating or preventing
PT tonsillitis, pneumonia, asthma and cystic fibrosis, emphysema, throat
PT cancer.

PS Claim 11; SEQ ID NO 585; 236pp; English.

XX The invention describes an isolated polypeptide (I) comprising an amino
CC acid sequence that is at least 90% identical to polypeptide fragment of
CC any one of 299 respiratory system antigen sequences (PS) and having
CC biological activity, polypeptide domain or epitope of PS, full-length
CC protein of PS, or variant, allelic variant or species homolog of PS. (I)

or a polynucleotide (II) encoding (I) is also useful for diagnosing a pathological condition or a susceptibility to a pathological condition in a subject which involves determining the presence or absence of mutation in (II) or determining the presence or amount of expression of (I) in a biological sample and diagnosing a pathological condition based on the result. The human respiratory system associated polynucleotides, the polypeptides encoded by them, and antibodies that immunospecifically bind these polypeptides are useful in diagnosis, treatment, prevention and/or prognosis of disorders of respiratory system such as throat disorders (e.g., vocal cord paralysis, tonsillitis, and laryngitis), lung disorders (e.g., pneumonia), allergic disorders, (e.g., asthma and eosinophilic pneumonitis), pleurisy, cystic fibrosis, emphysema, histiocytosis, sarcoidosis, nose disorders (rhinitis and sinusitis), neoplasms and/or cancers of respiratory tissues (e.g., throat cancer, lung cancer, and cancer of the nose). The polynucleotides are useful in gene therapy

Query Match 86.1%; Score 99; DB 7; Length 170;
Best Local Similarity 73.9%; Pred. No. 7.3e-09;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
|||||:|||||:|||||
Db 52 VLHIDLRRWADLLVAPLDANTL 74

RESULT 12
AAM39470
ID AAM39470 standard; protein; 204 AA.

XX AAM39470;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2615.

XX Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

XX 23-DEC-1999; 99US-00471275.

XX 21-JAN-2000; 2000US-00485725.

XX 25-APR-2000; 2000US-00552317.

XX 20-JUN-2000; 2000US-00598042.

XX 19-JUL-2000; 2000US-00620312.

XX 03-AUG-2000; 2000US-00653450.

XX 14-SEP-2000; 2000US-00662191.

XX 19-OCT-2000; 2000US-00693036.

XX 29-NOV-2000; 2000US-00727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58626.

XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
CC encoded polypeptides (AAM38642-AAM42213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activ/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders. Note: The sequence data for this patent did not form
CC part of the printed specification

XX SQ Sequence 204 AA;

Query Match 86.1%; Score 99; DB 4; Length 204;
Best Local Similarity 73.9%; Pred. No. 9e-09;
Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23

Db 86 VLHIDLRRWADLLVAPLDANTL 108

RESULT 13

AAB94179

ID AAB94179 standard; protein; 204 AA.

XX AAB94179;

XX 26-JUN-2001 (first entry)

XX Human protein sequence SEQ ID NO:14492.

DE Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX Homo sapiens.

XX EP1074617-A2.

XX 07-FEB-2001.

XX 28-JUL-2000; 2000EP-00116126.

XX 29-JUL-1999; 99JP-00248036.

XX 27-AUG-1999; 99JP-00300253.

XX 11-JAN-2000; 2000JP-00118776.

XX 02-MAY-2000; 2000JP-00183767.

XX 09-JUN-2000; 2000JP-00241899.

XX (HELI-) HELIX RES INST.

XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;

PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;

XX WPI; 2001-318749/34.

XX Primer sets for synthesizing polynucleotides, particularly the 5602 full-

PT length cDNAs defined in the specification, and for the detection and/or

PT diagnosis of the abnormality of the proteins encoded by the full-length

PT cDNAs.

XX Claim 8; SEQ ID NO 14492; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesising 5602 full-

CC length cDNAs defined in the specification. Where a primer set comprises:

CC (a) an oligo-dr primer and an oligonucleotide complementary to the

CC complementary strand of a polynucleotide which comprises one of the 5602

CC nucleotide sequences defined in the specification, where the

CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesising polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNA easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAH2445 to AAH95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 204 AA;

Query Match 86.1%; Score 99; DB 4; Length 204;
 Best Local Similarity 73.9%; Pred. No. 9e-09;
 Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
 ||||:|||||:|||||
 Db 86 VLHIDLRWADLLVAPLDANTL 108

RESULT 14

ABBI11631

ID ABBI1631 standard; peptide; 309 AA.

XX ABBI1631;

AC ABBI1631;

DT 11-JAN-2002 (first entry)

XX Human receptor molecule homologue, SEQ ID NO:2001.

KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
 KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
 KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
 KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
 KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
 KW chronic inflammatory condition; proliferative retinopathy;
 KW atherosclerosis; coronary heart disease; arterial ischaemia;
 KW bone disorder; osteoporosis; vascular growth disorder;
 KW tissue regeneration; wound healing; infection; immune disorder;
 KW cell culture; drug screening; gene therapy; antiinflammatory;
 KW antiasthmatic; antiarthritis; haemostatic; antiarteriosclerotic;
 KW cytostatic; osteoplastic; vasotropic; cardiant; virucide; antibacterial;
 KW antifungal; vulnery; antiulcer.

XX Homo sapiens.

XX WO200157188-A2.

XX 09-AUG-2001.

XX 05-FEB-2001; 2001WO-US003800.

XX 03-FEB-2000; 2000US-00496914.

XX 27-APR-2000; 2000US-00560875.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Drmanac RT;

XX WPI: 2001-457740/49.

XX N-PSDB; ABA08875.

XX Human proteins and DNA encoding sequences useful for preventing, treating
 FT or ameliorating a medical condition in a mammalian subject e.g. arthritis

PT and cancer.

XX Claim 20; Page 222; 1963pp; English.

CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
 CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
 CC invention also relates to vectors and recombinant host cells comprising a
 CC nucleotide of the invention, methods of producing the novel polypeptides,
 CC antibodies against the polypeptides, methods of detecting the nucleotides,
 CC or polypeptides in a sample, and methods of identifying compounds which
 CC bind to polypeptides of the invention. Although novel, many of the
 CC polypeptides of the invention have homology to known proteins, thereby
 CC giving an insight into their probable biological activities, and hence
 CC potential therapeutic applications. The polypeptides of the invention may
 CC have various activities, including cytokine, cell proliferation or cell
 CC differentiation activities; stem cell growth factor activity;
 CC haematopoiesis regulatory activity; tissue growth activity;
 CC immunomodulatory activity; activin- or inhibin-related activities;
 CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
 CC thrombolytic activities; receptor or ligand activities; or may be
 CC involved in oncogenesis, cancer cell proliferation or metastasis.
 CC Depending on their biological activities, polypeptides and nucleotides of
 CC the invention are useful for preventing, treating or ameliorating medical
 CC conditions, e.g., by protein or gene therapy. Such conditions include
 CC cancers, haematopoietic disorders (e.g., myeloid or lymphoid cell
 CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
 CC proliferative retinopathy, atherosclerosis, coronary heart disease,
 CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
 CC vascular growth. Polypeptides involved with tissue regeneration and
 CC repair (or nucleic acids encoding them) may be used to promote wound
 CC healing (e.g., of burns, incisions and ulcers), while those with
 CC immunomodulatory activities may be used in the treatment of viral,
 CC bacterial and fungal infections in addition to immune disorders.

CC Polypeptides with growth factor activity may be used in cell cultures to
 CC promote cell growth. For example, such polypeptides may be used to
 CC manipulate stem cells in culture to give rise to neuroepithelial cells
 CC that can be used to augment or replace cells damaged by illness,
 CC autoimmune disease or accidental damage. The polypeptides and nucleotides
 CC may also be used in the diagnosis of the above conditions, and in drug
 CC screening techniques. The present sequence represents a novel human
 CC polypeptide of the invention

SQ Sequence 309 AA;

Query Match 86.1%; Score 99; DB 4; Length 309;

Best Local Similarity 73.9%; Pred. No. 1.4e-08;

Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23

||||:|||||:|||||
 Db 121 VLHIDLRWADLLVAPLDANTL 143

RESULT 15

AAW41256

ID AAW41256 standard; protein; 309 AA.

XX AAW41256;

AC AAW41256;

XX 22-OCT-2001 (first entry)

XX Human polypeptide SEQ ID NO 6187.

KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

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XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US034263.
XX
XX 23-DEC-1999; 99US-00471275.
XX 21-JAN-2000; 2000US-00488725.
XX 25-APR-2000; 2000US-00552317.
XX 20-JUN-2000; 2000US-00598042.
XX 19-JUL-2000; 2000US-00620312.
XX 03-AUG-2000; 2000US-00653450.
XX 14-SEP-2000; 2000US-00662191.
XX 19-OCT-2000; 2000US-00693036.
XX 29-NOV-2000; 2000US-00727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
XX Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI: 2001-442253/47.
XX N-PSDB; AAI60412.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders such
XX as central nervous system injuries.
XX
XX Example 2; SEQ ID NO 6187; 10078pp; English.
XX
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and the
XX encoded polypeptides (AAM38642-AAM42213) with nootropic,
XX immunosuppressant and cytosstatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: Immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders. Note: The sequence data for this patent did not form
XX part of the printed specification
XX
XX Sequence 309 AA;
XX
XX Query Match 86.1%; Score 99; DB 4; Length 309;
XX Best Local Similarity 73.9%; Pred. NO. 1.4e-08;
XX Matches 17; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
XX
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XX Db 121 VLHIDLRRWADLLVAPLDANTL 143
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	78	67.8	427	US-09-328-352-5205	Sequence 5205, Ap
4	76	66.1	431	US-09-540-236-3536	Sequence 3536, Ap
5	71	61.7	405	US-09-252-991A-24057	Sequence 24057, A
6	69	60.0	399	US-09-710-279-2576	Sequence 2576, Ap
7	69	60.0	400	US-09-134-001C-4785	Sequence 4785, Ap
8	67	58.3	398	US-09-489-039A-10656	Sequence 10656, A
9	65	56.5	188	US-09-627-376-9	Sequence 9, Appl1
10	65	56.5	188	US-10-047-676B-9	Sequence 9, Appl1
11	65	56.5	418	US-09-543-681A-7435	Sequence 7435, Ap
12	61	53.0	183	US-09-583-110-4578	Sequence 4578, Ap
13	59	51.3	188	US-09-107-532A-6818	Sequence 6818, Ap
14	56	48.7	444	US-08-822-774-52	Sequence 52, Appl1
15	56	48.7	444	US-09-632-711-52	Sequence 52, Appl1
16	56	48.7	444	US-09-632-703B-52	Sequence 52, Appl1
17	56	48.7	444	US-09-632-702-52	Sequence 52, Appl1
18	56	48.7	444	US-09-399-003-52	Sequence 52, Appl1
19	48.5	42.2	339	US-09-248-796A-21067	Sequence 21067, A
20	48	41.7	850	US-09-583-110-4394	Sequence 4394, Ap
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25	46	40.0	403	US-09-399-003-19	Sequence 19, Appl1
26	45	39.1	501	US-09-934-868-56	Sequence 56, Appl1
27	45	39.1	689	US-09-107-532A-3870	Sequence 3870, Ap

28	44.5	38.7	141	4	US-09-270-767-61539	Sequence 61539, A
29	44.5	38.7	184	4	US-09-270-767-46002	Sequence 46002, A
30	44	38.3	45	4	US-09-270-767-60276	Sequence 60276, A
31	44	38.3	376	4	US-09-270-767-44809	Sequence 44809, A
32	44	38.3	641	4	US-09-252-991A-20102	Sequence 20102, A
33	43.5	37.8	426	4	US-09-252-991A-31959	Sequence 31959, Ap
34	43	37.4	163	4	US-09-107-532A-4269	Sequence 4269, Ap
35	43	37.4	797	4	US-09-134-000C-4997	Sequence 4997, Ap
36	43	37.4	1704	4	US-09-392-812A-2	Sequence 2, Appl1
37	42	36.5	150	4	US-09-270-767-46682	Sequence 46682, A
38	42	36.5	188	3	US-08-737-248-20	Sequence 20, Appl
39	42	36.5	264	4	US-09-586-106D-115	Sequence 115, Appl
40	42	36.5	372	4	US-09-489-039A-10774	Sequence 10774, A
41	42	36.5	2318	3	US-09-091-219-24	Sequence 24, Appl
42	42	36.5	2318	4	US-09-660-541-24	Sequence 24, Appl
43	41	35.7	106	3	US-09-376-330-25	Sequence 25, Appl
44	41	35.7	137	4	US-09-543-681A-5806	Sequence 5806, Ap
45	41	35.7	324	4	US-09-489-039A-10801	Sequence 10801, A

ALIGNMENTS

RESULT 1

US-09-248-796A-19036

; Sequence 19036, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 19036

; LENGTH: 459

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-19036

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Best Local Similarity 78.3%; Pred. No. 2.2e-08;

Matches 18; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVIITAPLSANTL 23

:|||:|||:|||:|||:|||

Db 367 ILHNLKRWADIMLIAPLSANTL 389

RESULT 2

US-09-248-796A-15512

; Sequence 15512, Application US/09248796A

; Patent No. 6747137

; GENERAL INFORMATION:

; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 15512

; LENGTH: 403

; TYPE: PRT

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; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (399),(400),(401)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-15512

Query Match      87.0%; Score 100; DB 4; Length 403;
Best Local Similarity 69.6%; Pred. No. 2.7e-08;
Matches 16; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY  1 VLHIELRRWADVMIIAPLSANTL 23
    ||||| ||||| :|||
Db   369 VLHIELRRWADLVVCPETANTL 391

RESULT 3
US-09-328-352-5205
; Sequence 5205, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5205
; LENGTH: 427
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5205

Query Match      67.8%; Score 78; DB 4; Length 427;
Best Local Similarity 61.9%; Pred. No. 0.00011;
Matches 13; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY  3 HIELRRWADVMIIAPLSANTL 23
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Db   90 HIELRWADLVVAPASCDYL 110

RESULT 4
US-09-540-236-3536
; Sequence 3536, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 3536
; LENGTH: 431
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-3536

Query Match      66.1%; Score 76; DB 4; Length 431;
Best Local Similarity 57.1%; Pred. No. 0.00024;
Matches 12; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY  3 HIELRRWADVMIIAPLSANTL 23
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Db   96 HITLKWADLVVAPASANTII 116

RESULT 5
US-09-252-991A-24057
; Sequence 24057, Application US/09252991A

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;; PRIOR FILING DATE: 1998-06-30
;; PRIOR APPLICATION NUMBER: US 60/085,131
;; PRIOR FILING DATE: 1998-05-12
;; PRIOR APPLICATION NUMBER: US 60/051,553
;; PRIOR FILING DATE: 1997-07-02
;; NUMBER OF SEQ ID NOS: 5322
;; SEQ ID NO 4578
;; LENGTH: 183
;; TYPE: PRT
;; ORGANISM: Streptococcus pneumoniae
US-09-583-110-4578

Query Match 53.0%; Score 61; DB 4; Length 183;
Best Local Similarity 52.2%; Pred. No. 0.026;
Matches 12; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
| | | | | : | | : | | : | | :
Db 69 VNHIELKKKADLFIVVPATANI 91

RESULT 13
US-09-107-532A-6818
; Sequence 6818, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6818:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc_feature
LOCATION: (B) LOCATION 1...188
SEQUENCE DESCRIPTION: SEQ ID NO: 6818:
US-09-107-532A-6818

Query Match 51.3%; Score 59; DB 4; Length 188;

Best Local Similarity 52.4%; Pred. No. 0.057;
Matches 11; Conservative 5; Mismatches 5; Indels 0; Gaps 0;
QY 3 HIELRWADVMIIAPLSANTL 23
| | | | | : | | : | | : | | :
Db 76 HIELAKQADLFIIAPATANI 96

RESULT 14
US-08-822-774-52
; Sequence 52, Application US/08822774
; Patent No. 6183997
; GENERAL INFORMATION:
; APPLICANT: HOGREFE, Holly
; TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
; TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,
; TITLE OF INVENTION: and Methods for Purifying and Identifying Same
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &
; ADDRESSEE: Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,774
FILING DATE: 21-MAR-1997
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:
NAME: KULIK, David J.
REGISTRATION NUMBER: 36,576
REFERENCE/DOCKET NUMBER: 1486/43163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 444 amino acids
TYPE: amino acid
TOPOLOGY: unknown

MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Escherichia coli
US-08-822-774-52

Query Match 48.7%; Score 56; DB 3; Length 444;
Best Local Similarity 44.0%; Pred. No. 0.46;
Matches 11; Conservative 7; Mismatches 3; Indels 4; Gaps 1;

QY 3 HIEL----RRWADVMIIAPLSANTL 23
| | | | | : | | : | | : | | :
Db 99 HIELGXXXXKQADLVILAPATADLI 123

RESULT 15
US-09-632-711-52
; Sequence 52, Application US/09632711
; Patent No. 6333165
; GENERAL INFORMATION:
; APPLICANT: HOGREFE, Holly
; TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)
; Extracts, PEF Protein Complexes, Isolated PEF Proteins,
; and Methods for Purifying and Identifying Same
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:

11

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 13:54:20 ; Search time 143 Seconds
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57.760 Million cell updates/sec

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Perfect score: 115
Sequence: 1 VLHILRRWADVMIAPLSANTL 23

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	111	96.5	168	US-10-425-115-322889	Sequence 322889, A
3	111	96.5	220	US-10-425-115-322884	Sequence 322884, A
4	111	96.5	220	US-10-425-115-322885	Sequence 322885, A
5	111	96.5	220	US-10-425-115-322895	Sequence 322895, A
6	111	96.5	220	US-10-425-115-322894	Sequence 322894, A
7	111	96.5	220	US-10-425-115-322896	Sequence 322896, A
8	111	96.5	226	US-10-425-114-63758	Sequence 63758, A
9	111	96.5	226	US-10-425-114-66204	Sequence 66204, A
10	111	96.5	226	US-10-425-114-66717	Sequence 66717, A
11	111	96.5	226	US-10-425-114-72163	Sequence 72163, A
12	111	96.5	226	US-10-425-114-72164	Sequence 72164, A
13	110	95.7	133	US-10-425-114-62134	Sequence 62134, A

14	110	95.7	204	15	US-10-424-599-190013	Sequence 190013, A
15	110	95.7	204	17	US-10-739-930-9355	Sequence 9355, Ap
16	110	95.7	220	16	US-10-437-963-133863	Sequence 133863, A
17	103	89.6	129	16	US-10-767-701-57336	Sequence 57336, A
18	99	86.1	170	9	US-09-764-860-585	Sequence 585, App
19	99	86.1	170	9	US-09-764-904-64	Sequence 64, Appl
20	99	86.1	170	14	US-10-091-548-64	Sequence 548, App
21	99	86.1	170	14	US-10-074-095-585	Sequence 585, App
22	99	86.1	170	14	US-10-212-872-585	Sequence 585, App
23	99	86.1	309	15	US-10-276-774-2001	Sequence 2001, Ap
24	65	56.5	188	13	US-10-047-676A-9	Sequence 9, Appli
25	65	56.5	188	17	US-10-790-914-9	Sequence 9, Appli
26	61	53.0	183	16	US-10-474-776-675	Sequence 675, App
27	56	48.7	425	15	US-10-335-977-5521	Sequence 5521, Ap
28	55	47.8	119	15	US-10-335-977-5519	Sequence 5519, Ap
29	51	44.3	228	9	US-09-895-913A-66	Sequence 66, Appl
30	48	41.7	405	14	US-10-156-761-14401	Sequence 14401, A
31	48	41.7	615	16	US-10-767-701-47307	Sequence 47307, A
32	48	41.7	850	16	US-10-474-776-421	Sequence 421, App
33	47	40.9	316	15	US-10-282-122A-73522	Sequence 73522, A
34	47	40.9	420	9	US-09-738-626-5274	Sequence 5274, Ap
35	46	40.0	157	15	US-10-424-599-216062	Sequence 216062, A
36	46	40.0	260	17	US-10-425-115-285975	Sequence 285975, A
37	46	40.0	261	17	US-10-425-115-286098	Sequence 286098, A
38	46	40.0	267	17	US-10-425-115-286030	Sequence 286030, A
39	46	40.0	270	17	US-10-425-115-286074	Sequence 286074, A
40	46	40.0	270	17	US-10-425-115-286087	Sequence 286087, A
41	46	40.0	292	17	US-10-425-115-301398	Sequence 301398, A
42	46	40.0	303	17	US-10-425-115-286063	Sequence 286063, A
43	46	40.0	364	17	US-10-779-597-113	Sequence 113, App
44	46	40.0	385	9	US-09-796-858-30	Sequence 30, Appl
45	45	39.1	85	17	US-10-425-115-243161	Sequence 243161, A

ALIGNMENTS

RESULT 1
US-10-425-114-62090
; Sequence 62090, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 62090
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3595-003-A8_FLI.pep
; US-10-425-114-62090

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Best Local Similarity 91.3%; Pred. No. 7, 5e-10;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLHILRRWADVMIAPLSANTL 23
Db 24 VLHILRRWADVMIAPLSANTL 46

RESULT 2
US-10-425-115-322889

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; Sequence 322899, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 322889
; LENGTH: 168
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(168)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57538C.1.pep
US-10-425-115-322889

Query Match          96.5%; Score 111; DB 17; Length 168;
Best Local Similarity 91.3%; Pred. No. 8.2e-10;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
Db 89 VLHIELRKWADVMVIAPLSANTL 111

RESULT 3
US-10-425-115-322884
; Sequence 322884, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57533C.1.pep
US-10-425-115-322884

Query Match          96.5%; Score 111; DB 17; Length 220;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
Db 89 VLHIELRKWADVMVIAPLSANTL 111

RESULT 4
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; Sequence 322885, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
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; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57534C.1.pep
US-10-425-115-322895

Query Match          96.5%; Score 111; DB 17; Length 220;
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QY 1 VLHIELRRWADVMIIAPLSANTL 23
Db 89 VLHIELRKWADVMVIAPLSANTL 111

RESULT 5
US-10-425-115-322894
; Sequence 322894, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 322894
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_57542C.1.pep
US-10-425-115-322894

Query Match          96.5%; Score 111; DB 17; Length 220;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
Db 89 VLHIELRKWADVMVIAPLSANTL 111

RESULT 6
US-10-425-115-322895
; Sequence 322895, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 322895
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; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_57543C.1.pep
US-10-425-115-322895

Query Match          96.5%; Score 111; DB 17; Length 220;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
Db 89 VLHIELRWADVMIIAPLSANTL 111

RESULT 7
US-10-425-115-322896
; Sequence 322896, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 322896
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MPT4577_57544C.1.pep
US-10-425-115-322896

Query Match          96.5%; Score 111; DB 17; Length 220;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
Db 89 VLHIELRWADVMIIAPLSANTL 111

RESULT 8
US-10-425-114-63758
; Sequence 63758, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63758
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3594-014-D7_FLI.pep
US-10-425-114-63758
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Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
Db 95 VLHIELRWADVMIIAPLSANTL 117

RESULT 9
US-10-425-114-66204
; Sequence 66204, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 66204
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4667-017-A10_FLI.pep
US-10-425-114-66204

Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
Db 95 VLHIELRWADVMIIAPLSANTL 117

RESULT 10
US-10-425-114-66717
; Sequence 66717, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 66717
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB4744-084-F10_FLI.pep
US-10-425-114-66717

Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADVMIIAPLSANTL 23
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Db          95 VLHIELRWADWVMIAPLSANTL 117
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US-10-425-114-72163
RESULT 11
; Sequence 72163, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72163
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-317-A6_FLI.pep
US-10-425-114-72163
Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADWVMIAPLSANTL 23
|||||||:|||||:|||||:|||||
Db 95 VLHIELRWADWVMIAPLSANTL 117

RESULT 12
US-10-425-114-72164
; Sequence 72164, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72164
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-384-D9_FLI.pep
US-10-425-114-72164
Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADWVMIAPLSANTL 23
|||||||:|||||:|||||:|||||
Db 95 VLHIELRWADWVMIAPLSANTL 117

RESULT 13
US-10-425-114-72165
; Sequence 72165, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 72165
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-384-D9_FLI.pep
US-10-425-114-72165
Query Match          96.5%; Score 111; DB 15; Length 226;
Best Local Similarity 91.3%; Pred. No. 1.1e-09;
Matches 21; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADWVMIAPLSANTL 23
|||||||:|||||:|||||:|||||
Db 95 VLHIELRWADWVMIAPLSANTL 117

RESULT 14
US-10-424-599-190013
; Sequence 190013, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: SOY Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 190013
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(204)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_142600C.1.pep
US-10-424-599-190013
Query Match          95.7%; Score 110; DB 15; Length 204;
Best Local Similarity 87.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRWADWVMIAPLSANTL 23
|||||||:|||||:|||||:|||||
Db 91 VLHIELRWADWVMIAPLSANTL 113

RESULT 15
US-10-739-930-9355
; Sequence 9355, Application US/10739930
; Publication No. US20040216190A1
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; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH
; FILE OF INVENTION: PLANTS AND USES THEREOF FOR PLANT IMPROVEMENT
; FILE REFERENCE: 38-21(53377)B
; CURRENT APPLICATION NUMBER: US/10/739,930
; CURRENT FILING DATE: 2003-12-18
; NUMBER OF SEQ ID NOS: 11088
; SEQ ID NO 9355
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(204)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: GLYMA-23APR03-C7627_42.p
US-10-739-930-9355
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Query Match 95.7%; Score 110; DB 17; Length 204;
Best Local Similarity 87.0%; Pred. No. 1.5e-09;
Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 VLHIELRWADVMIIAPLSANTL 23
Db 91 VLHIELRWADIMVIAPLSANTL 113
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Search completed: December 23, 2004, 14:20:54
Job time : 147 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 23, 2004, 13:00:33 ; Search time 188 seconds
(without alignments)
70.392 Million cell updates/sec

Title: US-09-868-300-8_COPY_96_118
Perfect score: 115
Sequence: 1 VLHIELRRWADVMIAPLSANTL 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt_02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	115	100.0	201	1 HL3B_ARATH	P94063 arabidopsis
2	111	96.5	209	1 HL3A_ARATH	Q9swe5 arabidopsis
3	111	96.5	209	2 AAT41764	Aat41764 arabidops
4	108	93.9	257	2 Q9HEH6	Q9heh6 neurospora
5	108	93.9	260	2 Q7RVD1	Q7rvd1 neurospora
6	107	93.0	183	2 Q7OH41	Q7oh41 fowlpox vir
7	107	93.0	183	2 Q9J5A8	Q9j5a8 fowlpox vir
8	107	93.0	183	2 CAE52655	Caes52655 fowlpox v
9	107	93.0	538	2 Q6FTJ7	Q6ftj7 candida gla
10	106	92.2	120	2 Q9AVS8	Q9avs8 picea abies
11	106	92.2	488	2 Q6CCV1	Q6ccv1 yarrowia li
12	106	92.2	562	1 S1S2_YEAST	P36024 saccharomyc
13	106	92.2	571	2 Q6FKN2	Q6fkn2 candida gla
14	106	92.2	648	2 Q7SEB1	Q7seeb1 ashbya goss
15	106	92.2	648	2 AAS50506	Aas50506 ashbya go
16	106	92.2	649	2 Q6CJS7	Q6cjs7 kluyveromyc
17	106	92.2	674	1 VHS3_YEAST	Q08438 saccharomyc
18	104	90.4	203	2 Q6PEQ5	Q6peq5 brachydanio
19	104	90.4	203	2 AAH59622	Aah59622 brachydan
20	104	90.4	559	2 Q6BR16	Q6br16 debaryomyc
21	103	89.6	184	2 Q6VZK6	Q6vzk6 canarypox v
22	103	89.6	184	2 AAR83487	Aar83487 canarypox
23	102	88.7	48	2 Q99J33	Q99j33 mus musculu
24	102	88.7	204	2 Q8BZB2	Q8bz2 mus musculu
25	102	88.7	530	2 Q759W6	Q759w6 ashbya goss
26	102	88.7	530	2 AAS52077	Aas52077 ashbya go
27	101	87.8	531	1 S1S2_CANTR	Q12600 candida tro
28	101	87.0	543	2 Q6CWR1	Q6cwr1 kluyveromyc
29	99	86.1	127	2 Q9HCL7	Q9hcl7 homo sapien
30	99	86.1	204	2 Q96CD2	Q96cd2 homo sapien
31	99	86.1	204	2 Q96SX0	Q96sx0 homo sapien

32	99	86.1	204	2 AAQ89207	Aaq89207 homo sapi
33	96	83.5	571	1 YK18_YEAST	P36076 saccharomyc
34	96	83.5	607	2 Q6BPI6	Q6bpi6 debaryomyc
35	95	82.6	185	2 Q8IAZ8	Q8iaz8 plasmodium
36	94	81.7	179	2 Q7RRZ6	Q7rrz6 plasmodium
37	92	80.0	237	2 Q9I988	P91988 caenothabdi
38	92	80.0	625	2 Q9UTI7	Q9uti7 schizosacch
39	91	79.1	191	2 Q8MKK3	Q8mkk3 drosophila
40	91	79.1	415	2 Q6C6T7	Q6c6t7 yarrowia li
41	90	78.3	191	2 Q7PZN2	Q7pzn2 anopheles g
42	89	77.4	410	2 Q8YSH4	Q8yeh4 anabaena sp
43	88	76.5	544	2 Q8FL89	Q8fli89 candida gla
44	83	72.2	418	2 Q7V359	Q7v359 prochloroco
45	80	69.6	402	1 DFP_SYNY3	P73881 s coenzyme

ALIGNMENTS

RESULT 1
HL3B_ARATH
ID HL3B_ARATH STANDARD; PRT; 201 AA.
AC P94063; Q9LP62;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Probable phosphopantothencysteine decarboxylase (EC 4.1.1.36)
DE (Halotolerance protein Hal3b) (AtHal3b).
GN Name=HAL3B; OrderedLocusNames=At1g48610; ORFNames=T1N15.24;
OS Arabidopsis thaliana (Mouse-ear cress);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RS SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=cv. Columbia;
RX MEDLINE=20117504; PubMed=10652125;
RA Espinosa-Ruiz A., Belles J.M., Serrano R., Cullane-Macia F.A.;
RT "Arabidopsis thaliana AtHAL3: a flavoprotein related to ealt and
RT osmotic tolerance and plant growth.",
RL Plant J. 20:529-539(1999).
[2]
SEQUENCE FROM N.A.
RN
RP STRAIN=cv. Columbia;
RX MEDLINE=21016719; PubMed=11130712; DOI=10.1038/35048500;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
RA Dunn P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldenmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Krenetskaia I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,
RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RT thaliana".
RL Nature 408:816-820(2000).
CC -!- FUNCTION: Involved in plant growth and salt and osmotic tolerance.
CC Catalyzes the decarboxylation of 4'-phosphopantothencysteine to
CC 4'-phosphopantetheine, a key step in coenzyme A biosynthesis. The
CC enzyme is also able to decarboxylate pantothencysteylamine to
CC pantothencysteamine (By similarity).
CC -!- CATALYTIC ACTIVITY: N-[(R)-4'-phosphopantothencyl]-L-cysteine =
CC pantothencine 4'-phosphate + CO(2).
CC -!- COFACTOR: Binds 1 FMN per subunit (By similarity).

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CC -I- SUBUNIT: Homotrimer (By similarity).
CC -I- TISSUE SPECIFICITY: Expressed in roots, shoots, leaves, flowers,
CC developing siliques and seeds.
CC -I- INDUCTION: By salt stress.
CC -I- SIMILARITY: Some, to yeast and C.tropicalis SIS2/HAL3 and yeast
CC YKL088W.
CC -I- SIMILARITY: Belongs to the HFCD (homo-oligomeric flavin containing
CC Cys decarboxylase) superfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; U80192; AAB53106.1; -.
CC EMBL; AC020889; AAF79709.1; ALT_INIT.
CC HSSP; Q9SW55; IMVL.
CC InterPro; IPR003382; Flavoprotein.
CC TIGRFAMs; TIGR01847; bacteriocin_sig; 1.
CC Flavoprotein; FMN; Lyase.
CC ACT SITE 90
CC SEQUENCE 201 AA; 22415 MW; 7962655E408FA64C CRC64;
CC -----
Query Match 100.0%; Score 115; DB 1; Length 201;
Best Local Similarity 100.0%; Pred. No. 7,5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLHILRRWADYMIAPLSANTL 23
DB 80 VLHILRRWADYMIAPLSANTL 102
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RESULT 2
HL3A_ARATH
ID HL3A_ARATH STANDARD; PRT; 209 AA.
AC Q9SW55;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Phosphopantothencysteine decarboxylase (EC 4.1.1.36) (Halotolerance
DE Protein Hal3a) (AtHal3a) (PPDCoC).
DE Name=HAL3A; OrderedLocNames=At3g18030; ORFNAMES=MBG14.2;
DE Arabidopsis thaliana (Mouse-ear cress).
DE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DE Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
DE eurosid II; Brassicales; Brassicaceae; Arabidopsis.
DE NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND INDUCTION.
RC STRAIN=cv. Columbia;
RX MEDLINE=20117504; PubMed=10652125;
RA Espinosa-Ruiz A., Belles J.M., Serrano R., Cullianez-Macia F.A.;
RT "Arabidopsis thaliana ATHAL3: a flavoprotein related to salt and
RT osmotic tolerance and plant growth.";
RL Plant J. 20:529-539(1999).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 P1, TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [3]
RN CHARACTERIZATION OF ACTIVITY, AND MUTAGENESIS OF HIS-90.
RX PubMed=11279129; DOI=10.1074/jbc.M100776200;
RA Kupke T., Hernandez-Acosta P., Steinbacher S., Cullianez-Macia F.A.;
RT "Arabidopsis thaliana flavoprotein ATHAL3a catalyzes the

```

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RT decarboxylation of 4'-Phosphopantothencysteine to 4'-
RT phosphopantetheine, a key step in coenzyme A biosynthesis.";
RN J. Biol. Chem. 276:19190-19196(2001).
RL [4]
RP CHARACTERIZATION OF ACTIVITY, AND MUTAGENESIS OF VAL-30; ILE-33;
RP LYS-34; ARG-95; ASN-142; MET-145; ALA-174; CYS-175; ASP-177; GLY-179
RP AND GLY-181.
RP PubMed=11923307; DOI=10.1074/jbc.M201557200;
RX Hernandez-Acosta P., Schmid D.G., Jung G., Cullianez-Macia F.A.,
RX Kupke T.;
RA "Molecular characterization of the Arabidopsis thaliana flavoprotein
RA ATHAL3a reveals the general reaction mechanism of 4'-
RA phosphopantothencysteine decarboxylases.";
RL J. Biol. Chem. 277:20490-20498(2002).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RP MEDLINE=20444410; PubMed=10986463;
RX Albert A., Martinez-Ripoll M., Espinosa-Ruiz A., Yenush L.,
RX Cullianez-Macia F.A., Serrano R.;
RT "The X-ray structure of the FMN-binding protein ATHAL3 provides the
RT structural basis for the activity of a regulatory subunit involved in
RT signal transduction.";
RL Structure 8:961-969(2000).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.21 ANGSTROMS) OF MUTANT SER-175.
RX MEDLINE=22503127; PubMed=12614618; DOI=10.1016/S0022-2836(03)00092-5;
RA Steinbacher S., Hernandez-Acosta P., Bieseler B., Blaesse M.,
RA Huber R., Cullianez-Macia F.A., Kupke T.;
RT "Crystal structure of the plant PPC decarboxylase ATHAL3a complexed
RT with an ene-thiol reaction intermediate.";
RL J. Mol. Biol. 327:193-202(2003).
CC -I- FUNCTION: Involved in plant growth and salt and osmotic tolerance.
CC Catalyzes the decarboxylation of 4'-phosphopantothencysteine to
CC 4'-phosphopantetheine, a key step in coenzyme A biosynthesis. The
CC enzyme is also able to decarboxylate pantothencysteine to
CC pantothencylsteamine.
CC -I- CATALYTIC ACTIVITY: N-[(R)-4'-phosphopantothenoil]-L-cysteine =
CC pantothene 4'-phosphate + CO(2).
CC -I- COFACTOR: Binds 1 FMN per subunit.
CC -I- PATHWAY: Coenzyme A (CoA) biosynthesis; third step.
CC -I- SUBUNIT: Homotrimer.
CC -I- TISSUE SPECIFICITY: Expressed in roots, shoots, leaves, flowers,
CC developing siliques, and seeds with highest expression in seed
CC embryo and phloem.
CC -I- INDUCTION: By salt stress.
CC -I- SIMILARITY: Some, to yeast and C.tropicalis SIS2/HAL3 and yeast
CC YKL088W.
CC -I- SIMILARITY: Belongs to the HFCD (homo-oligomeric flavin containing
CC Cys decarboxylase) superfamily.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF166262; AAD51616.1; -.
CC EMBL; AB026641; BAB01331.1; -.
CC PDB; 1E20; X-ray; A=1-209.
CC PDB; 1MVL; X-ray; A=1-209.
CC PDB; 1MVN; X-ray; A=1-209.
CC InterPro; IPR003382; Flavoprotein.
CC Pfam; PF02441; Flavoprotein; 1.
CC 3D-structure; Flavoprotein; FMN; Lyase.
CC ACT SITE 90
CC MUTAGEN 30 90 V->I: No effect on activity.
CC MUTAGEN 33 33 I->L,V: No effect on activity.
CC MUTAGEN 34 34 K->N,R: No effect on activity.
CC MUTAGEN 34 34 K->Q: Small decrease of activity.
CC MUTAGEN 90 90 H->N: Complete loss of activity.
CC MUTAGEN 95 95 R->Q: Very low activity. Can reduce the

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Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000272; EAA31992.1; -.
DR InterPro; IPR003382; Flavoprotein.
DR Pfam; PF02441; Flavoprotein; 1.
SQ SEQUENCE 260 AA; 28662 MW; BDF01BD90726537A CRC64;

Query Match 93.9%; Score 108; DB 2; Length 260;
Best Local Similarity 78.3%; Pred. No. 1.5e-09;
Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
DB 120 ILHIELRRWADILVVAFLSANTL 142
:|||||:|||||:|||||:|||||:|||||

RESULT 6
Q70H41 PRELIMINARY; PRT; 183 AA.
ID Q70H41
AC Q70H41;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein fp9.114.
GN Name=fp9.114;
OS Fowlpox virus (isolate HP-438[Munich]).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus
OC NCBI_TaxID=10263;
OX [1]
RN SEQUENCE FROM N.A.
RA Skinner M.A., Laidlaw S.M.;
RT "Comparison of the genome sequence of FP9, an attenuated, tissue
RT culture-adapted European fowlpox virus, with those of virulent
RT American and European viruses.";
RL J. Gen. Virol. 85:305-322(2004).
RL EMBL; AJ581527; CAB52855.1; -.
DR InterPro; IPR003382; Flavoprotein.
DR Pfam; PF02441; Flavoprotein; 1.
KW Hypothetical protein.
SQ SEQUENCE 183 AA; 20778 MW; 090E039BC0CE27D3 CRC64;

Query Match 93.0%; Score 107; DB 2; Length 183;
Best Local Similarity 91.3%; Pred. No. 1.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIIAPLSANTL 23
DB 72 VLHIELRRWADVFIIAPLTANTL 94
:|||||:|||||:|||||:|||||:|||||

RESULT 7
Q9J5A8 PRELIMINARY; PRT; 183 AA.
ID Q9J5A8
AC Q9J5A8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE ORF FPV114 HAL3 domain.
GN Name=FPV114;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OC NCBI_TaxID=10261;
OX [1]
RN SEQUENCE FROM N.A.
RA MEDLINE=20193820; PubMed=10729156;
RX MEDLINE=20193820; PubMed=10729156;


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RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Franchin L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,
RA Hantraye F., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004);
DR EMBL; CR380953; CAG59374.1; --
DR InterPro; IPR003382; Flavoprotein.
DR Pfam; PF02441; Flavoprotein; 1.
SQ SEQUENCE 538 AA; 58993 MW; 669E74BF4E2436F7 CRC64;

Query Match 93.0%; Score 107; DB 2; Length 538;
Best Local Similarity 82.6%; Pred. No. 4.7e-09;
Matches 19; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIAPLSANTL 23
Db 357 VLHIELRRWADVMIAPLSANTL 379

RESULT 10
Q9AVS8 PRELIMINARY; PRT; 120 AA.
AC Q9AVS8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative halotolerance protein HAL3 homolog (Fragment).
GN Name=ppA0038;
OS Picea abies (Norway spruce) (Picea excelsa).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
OX NCBI_TaxID=3329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Karst.;
RA Schubert R., Mueller-Starck G., Riegel R.;
RT "Development of EST-PCR markers and monitoring their intrapopulation
RT genetic variation in Picea abies (L.) Karst.";
RL Theor. Appl. Genet. 103:1223-1231(2001).
DR EMBL; AJ271130; CAC27336.1; --
DR HSP; Q98WE5; 1E20.
DR InterPro; IPR003382; Flavoprotein.
DR Pfam; PF02441; Flavoprotein; 1.
FT NON_TER 1
SQ SEQUENCE 120 AA; 13064 MW; 4164223419A49FDA CRC64;

Query Match 92.2%; Score 106; DB 2; Length 120;
Best Local Similarity 87.0%; Pred. No. 1.4e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIAPLSANTL 23
Db 6 VLHIELRRWADVMIAPLSANTL 28

RESULT 11
Q6CCV1 PRELIMINARY; PRT; 488 AA.
ID Q6CCV1;
AC Q6CCV1;
DT 01-OCT-2004 (TrEMBLrel. 28, Created)
DT 01-OCT-2004 (TrEMBLrel. 28, Last sequence update)

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DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|Q12600 Candida tropicalis SIS2 protein.
GN ORFNames=VALIO06281g;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RG GENOLEVURES;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talla E.,
RA Goffard N., Franchin L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissame A., Boyer J., Cattolico L., Confaniolero F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA Swennene D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zenlou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpetti C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIB99;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382129; CAG81812.1; --
SQ SEQUENCE 488 AA; 54852 MW; 8F8BEF5CBA9314CB CRC64;

Query Match 92.2%; Score 106; DB 2; Length 488;
Best Local Similarity 82.6%; Pred. No. 6.3e-09;
Matches 19; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLHIELRRWADVMIAPLSANTL 23
Db 260 VLHIELRRWADVMIAPLSANTL 282

RESULT 12
SIS2_YEAST
ID SIS2_YEAST STANDARD; PRT; 562 AA.
AC P36024;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE SIS2 protein (Halotolerance protein HAL3).
GN Name=SIS2; Synonyms=HAL3; OrderedLocusNames=YKR072C;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95220693; PubMed=7705654;
RA di Como C.J., Bose R., Arndt K.T.;
RT "Overexpression of SIS2, which contains an extremely acidic region,
RT increases the expression of SWI4, CLN1 and CLN2 in sit4 mutants.";
RL Genetics 139:95-107(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC Pohl T.M., Pohl F.M.;
RA Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE=96009574; PubMed=7565698;
RA Ferrando A., Kron S.J., Rios G., Fink G.R., Serrano R.;
RT "Regulation of cation transport in Saccharomyces cerevisiae by the

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RA	Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA	Boisrame A., Boyer J.J., Cattolico L., Confanioleri F., de Baruvier A.,
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA	Karrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA	Nicaud J.M., Nikolski M., Ootas S., Ozler-Kalogeropoulos O.,
RA	Pallenz S., Potier S., Richard G.F., Straub M.L., Suleau A.,
RA	Svennens D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA	Zenou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA	Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
RA	Wincker P., Souciet J.L.;
RT	"Genome evolution in yeasts.";
RL	Nature 430:35-44(2004).
DR	EWBL; CR380958; CG62186.1; -.
DR	InterPro; IPR003382; Flavoprotein.
DR	Pfam; PF02441; Flavoprotein; 1.
SQ	SEQUENCE 571 AA; 63117 MW; CD56BDE5ECAECE CRC64;
Query Match	92.2%; Score 106; DB 2; Length 571;
Best Local Similarity	78.3%; Pred.No. 7.4e-09;
Matches 18; Conservative	5; Mismatches 0; Indels 0; Gaps 0;
Qy	1 VLHIELRRWADVMIIAPLSANTL 23 :::
Dd	380 VLHIELRRWADILVAVPLTANTL 402
RESULT 14	
Q75EE1	PRELIMINARY; PRT; 648 AA.
ID AC Q75EE1;	
RP STRAIN=ATCC 10895;	
RX PubMed=15001715;	
RC Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,	
RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavlier A.,	
RA Gaffney T.D., Philippsen P.;	
RT "the Ashbya gossypii genome as a tool for mapping the ancient	
RL Saccharomyces cerevisiae Genome."	
RL Science 304:304-307(2004).	
DR EWBL; AE016881; AAS50506.1; -.	
DR AGD; AAR140W; -.	
DR InterPro; IPR003382; Flavoprotein.	
DR Pfam; PF02441; Flavoprotein; 1.	
SQ SEQUENCE 648 AA; 68696 MW; 1FD5D9CB9F0375D3 CRC64;	
Query Match	92.2%; Score 106; DB 2; Length 648;
Best Local Similarity	78.3%; Pred.No. 8.5e-09;
Matches 18; Conservative	5; Mismatches 0; Indels 0; Gaps 0;
Qy	1 VLHIELRRWADVMIIAPLSANTL 23 :::
Dd	449 VLHIELRRWADILVAVPLTANTL 471
RESULT 15	
AAS50506	PRELIMINARY; PRT; 648 AA.
ID AAS50506	
AC AAS50506;	
DT 23-APR-2004 (TrEMBLrel. 27, Created)	
DT 23-APR-2004 (TrEMBLrel. 27, Last sequence update)	
DE 23-APR-2004 (TrEMBLrel. 27, Last annotation update)	
DE AAR140WP.	

GN AAR140W.
 OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
 OX NCBI_TaxID=33169;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 10895;
 RX PubMed=15001715;
 RA Dietrich F.S., Voegelé S., Brachat S., Lerch A., Gates K., Steiner S.,
 RA Mohr C., Pohlmann R., Luedi P., Choi S., Wing R.A., Flavier A.,
 RA Caffney T.D., Philippsen P.;
 RT "The Ashbya gossypii genome as a tool for mapping the ancient
 RT Saccharomyces cerevisiae genome."; Science 304:304-307(2004).
 RL Science 304:304-307(2004).
 DR EMBL; AE016881; AAS0506.1; --
 SQ SEQUENCE 648 AA; 68696 MW; 1FD5D9CB9F0375D3 CRC64;

Query Match 92.2%; Score 106; DB 2; Length 648;
 Best Local Similarity 78.3%; Pred. NO. 8.5e-09;
 Matches 18; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLHIELRRWADYMIAPLSANTL 23
 Db 449 VLHIELRRWADILVWAPLTANTL 471

Search completed: December 23, 2004, 13:57:28
 Job time : 191 secs

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